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Cancer Risk Assessment by Rural and Appalachian Family Medicine Physicians

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Abstract

Context—Challenges to the identification of hereditary cancer in primary care may be more pronounced in rural Appalachia, a medically underserved region.

Purpose—To examine primary care physicians' identification of hereditary cancers.

Methods—A cross-sectional survey was mailed to family physicians in the midwestern and southeastern United States, stratified by rural/non-rural and Appalachian/non-Appalachian practice location (N=176). Identification of hereditary breast-ovarian cancer (BRCA1/2), hereditary non-polyposis colon cancer (HNPCC), and other hereditary cancers was assessed.

Findings—Less than half of physicians (45%) reported having patients with cancer genetic testing. Most (70%) correctly identified the BRCA1/2-relevant scenario; 49% correctly identified the HNPCC-relevant scenario. Factor analysis of psychosocial variables revealed 2 factors: Confidence (knowledge, comfort, confidence) and Importance (responsible, important, effective, need) of identifying hereditary cancer. Greater confidence was associated with use of 3 generation pedigree in taking family history. Greater knowledge and access to genetic services were associated with use of genetic testing. More recent graduation year, greater knowledge, and greater confidence were associated with identifying the BRCA1/2-relevant scenario. Greater knowledge and confidence were associated with identifying the HNPCC-relevant scenario.

Conclusions—Although rural Appalachian physicians do not differ in ability to identify high risk individuals, access barriers may exist for genetic testing. Interventions are needed to boost physician confidence in identifying hereditary cancer and to improve availability and awareness of availability of genetic services.

Keywords

hereditary cancer; physicians; primary care; psychosocial factors; Appalachian region

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Context

Many have discussed potential challenges to identification of hereditary cancer syndromes (HCs) in primary care.[1] HCs are a significant health risk due to their association with increased risk of cancer. For example, hereditary non-polyposis colon cancer (HNPCC) has been associated with a 70–90% lifetime risk of colon cancer.[2] Hereditary mutations in *BRCA1/2* have been associated with a 60–85% lifetime risk of breast cancer.[3] Features of HCs include: early age of cancer onset, multiple primary cancers, multiple family members affected, and association with an identified hereditary genetic mutation or a particular set of diagnostic criteria. Approximately 10% of cancers are believed hereditary.[4] This does not include family members who may also have an HC. Thus, HCs affect a large number of people, require earlier onset of screening, more frequent screening, and often, specific types of screening.

Primary care physicians (PCPs) play a critical role in the appropriate identification of individuals with HCs. Identifying individuals involves collecting and interpreting family history information. Construction and interpretation of a three-generation pedigree (3GP) is standard of care in fields such as oncology and medical genetics[5, 6] and is widely recommended in primary care.[7, 8] Yet many physicians do not routinely collect such family history information.[9–13] Further, studies have noted that 1–40% of physicians surveyed had patients with genetic testing in the past year.[14–16] Consistent with findings in other parts of the United States, PCPs in rural areas may be unprepared to identify individuals with HCs due to competing demands, shortages of PCPs, less accessibility of health services, inability to pay for health services, and lower education levels of patients.[16–19] These issues are particularly salient for rural Appalachian Kentucky and Ohio, a geo-politically designated region that has poorer access to care and lower socioeconomic status.[20, 21]

In addition to access barriers, physician knowledge and having attitudes that support the identification of HCs is important. If physicians believe that identifying such cancers is not important, not effective, not needed, not their role, or if physicians lack confidence in or are not comfortable with identifying individuals with HCs, appropriate identification may not occur. Physician knowledge deficits regarding genetics have been identified, such as difficulty determining who was at risk in an affected family, not regularly reading articles about genetic testing, making inappropriate recommendation for genetic testing, and reporting low knowledge of genetics.[22–26] Further, confidence is an important factor in the identification of HCs, with those practicing less than 20 years and specialists (i.e., obstetrician-gynecologists) being more confident than those practicing longer and PCPs, respectively.[12] As far as responsibility, studies conducted in Europe found that the majority of PCPs believed that calculating risk of family history of cancer was their role and were confident in assessing and counseling about risk.[10, 27, 28] It is difficult to know how these results generalize to the US, which has a different population with a different medical system.

Physicians in the US may be less confident in interpreting a family history of cancer for several reasons, including the variety of available guidelines,[29, 30] fear of patient insurance discrimination,[18, 31] and a belief that there is no clinical utility of genetic testing.[32] Given limited knowledge of and attitudes inconsistent with genetic testing, it is not surprising that physicians would have difficulty identifying individuals with HCs. The purpose of the current study was to understand PCP identification of HCs in rural Appalachia. Specifically, methods to assess risk (i.e., construction of a 3GP), current use of genetic testing practice, and correct identification of HCs through a scenario were assessed. We hypothesized that PCPs in rural and Appalachian practice locations would have more difficulty identifying

HCs. Further, PCPs with greater knowledge and with attitudes consistent with identification would be better able to identify HCs.

Methods

Participants were family medicine physicians and were members of the Kentucky Ambulatory Network (KAN), listed in the Kentucky Board of Medical Licensure (KBML), members of the Ohio State University Primary Care Network (OSUPCN), and/or listed in the Ohio Medical Board of Licensure (OBML). Family medicine physicians were chosen because (1) they represent the largest group of PCPs in Kentucky and Ohio, (2) they are represented throughout both states, and (3) they see all ages of patients. KAN and OSUPCN are practice-based research networks of clinicians who may be more motivated to be involved in research, more informed, and more up-to-date than non-practice-based research network members; thus, a population-based sample to supplement the KAN and OSUPCN was chosen from the KBML and OBML.

Our goal was to attain a sample size of 200, stratified by rural Appalachian, non-rural Appalachian, rural non-Appalachian, and non-rural non-Appalachian physicians. County was used to determine whether the physician practiced in a federally designated Appalachian region[20] or a rural area (non-rural=Rural-Urban Continuum Codes[RUCCs] 1–6; rural=RUCCs 7–9), as our goal was to examine physician identification of HCs in the most rural of areas.[33] To achieve adequate sample sizes to perform statistical analyses, some cells were over-sampled. Family practice physicians from the KAN and OSUPCN were exhaustively sampled. Members of KAN and OSUPCN were removed from the potential participants from the KBML and OBML listings. Remaining physicians listed by the KBML and OBML were randomly sampled within strata (e.g., rural/non-rural, Appalachian/non-Appalachian) by drawing numbers (corresponding to physician names) out of a hat.

In 2006–2007, physicians were mailed a survey packet, which included: (1) a letter to physicians, (2) a reply envelope, and (3) the survey. Genetic testing ordered (expanded from a previous study[14]) and methodologies to document family history were assessed. Two hypothetical clinical scenarios were presented and used to assess behavior regarding the identification and management of individuals with F/HCS and genetic testing uptake (see Supplementary Figure, available online). A scenario methodology has been used previously to assess knowledge of HNPCC, risk of familial breast and colorectal cancer, and referral recommendations.[10, 13, 34] Time to complete the 8-page survey was approximately 15 minutes. Physicians were compensated $50 upon return of a completed survey.

Mailing of packets was staggered to facilitate follow-up. Approximately two weeks after distribution of the survey, follow-up telephone calls were made to non-respondents to confirm receipt of the survey and encourage survey completion; additional survey packets were mailed, if not received. Following the initial mailing, an additional mailing was sent to non-respondents. Again, non-respondents to this additional mailing were contacted by telephone two weeks after survey distribution to encourage survey completion.

Measures

The survey included: (1) predictor variables (demographics and psychosocial factors), and (2) outcome variables (identification). Demographic information included gender, birth year, graduation year, license year, ZIP code to determine Appalachian (yes/no) and rural practice location (yes/no). In addition, research membership (KAN, OSUPCN, none), practice type (university-affiliated, community-based), and physician's perception of access to medical genetics services were assessed on a five-point scale (very easy-very difficult).

A psychosocial scale of eight items addressed physician factors relevant to the identification of individuals with or at risk for HC (Table 1). Mean scales were computed as a function of factor-analyzed scales. Ten statements were included to assess factual knowledge of HC (Table 1). Three were general questions about HC, three items relevant to hereditary colon cancer, and four items relevant to hereditary breast-ovarian cancer. Number of correct responses was summed to create a knowledge score.

Physicians were asked, "Do you use any methods to determine if your patients have a form of familial cancer?" and were instructed to check all options that applied. Responses included: intake questionnaire, intake interview, construction of 3GP, and do not collect. Physicians were also asked, "To your knowledge, have any of your patients been tested for any of the following genetic mutations (whether ordered by you or a specialist) associated with hereditary cancer?" and were instructed to check all options that applied. Response options included a variety of more common (e.g., *BRCA1/BRCA2, MLH1/MSH2/MSH6/PMS1/PMS2, p53, NF1/NF2*) and rare (e.g., *BLM, XPA*) genetic mutations associated with cancer, as well as the option of responding, don't know, none of these, or other. Below each of the scenarios (see Supplementary Figure, available online), physicians were asked, "Which, if any, of the following syndromes is the most relevant to this scenario?" Response options included: BRCA1/BRCA2 Hereditary Breast Ovarian Cancer (HBOC), Li-Fraumeni Syndrome, Hereditary Non-Polyposis Colon Cancer (HNPCC, Lynch syndrome), Cowden Syndrome, Familial Adenomatous Polyposis (FAP), None of these are relevant, or Don't know. HBOC was the correct answer for scenario I, and HNPCC, Lynch syndrome was relevant for scenario II.

Statistical Analysis

Means, standard deviations, and frequencies were used to describe the data and examine the data for suitability of parametric analyses. Separate Principle Components Analyses with Varimax rotation were conducted for the psychosocial items associated with physician identification of HC and for the knowledge items. Internal consistencies were computed with Cronbach alphas. Associations of demographic and psychosocial factors with each outcome (use of 3GP, use of genetic testing, and correct identification of scenarios) were evaluated. T-tests for continuous variables and chi-square tests for categorical variables were used to compare the demographic and (self-assessment) factors of respondents with each outcome. For each outcome, a multivariable logistic regression model was fit to the data using all demographic and psychosocial variables that were associated with the outcome in univariable analysis. In the multivariable model, variables with $p>.05$ were then removed sequentially to obtain a final model. Due to the large proportion of missing values, year of birth was not used in any models.

Results

A total of 176 responses were received (40% response rate). Non-rural, non-Appalachian had the highest participation rate (56%, 56/115) followed by non-rural, Appalachian physicians (39%, 47/122); rural, non-Appalachian physicians (37%, 33/90); and rural, Appalachian physicians (36%, 40/111). Most physicians felt that access to a medical geneticist was somewhat or extremely difficult (66%). Most also used some form of family history collection (76%), but did not use a 3-generation pedigree (92%). Less than half of physicians (45%) reported having patients with cancer genetic testing. Most (70%) correctly identified the BRCA1/2-relevant scenario; 49% correctly identified the HNPCC-relevant scenario. The modal number of knowledge questions correct was 6, with none having all 10 correct.

Table 1 presents the factor analyses of psychosocial factors related to identification of HCs and of the knowledge items. For the psychosocial factors, two factors were identified with eigenvalues>1, which were labeled confidence (3 items) and importance (4 items). Item one was dropped, as it was not closely related to either factor. For the knowledge items, one factor had an eigenvalue>1. Internal consistency for the scales was very good.

Demographic and psychosocial factors by each outcome were identified, with significant univariable t-test or chi-square test results indicated (see Supplementary Table, available online). Final (potentially) multivariable models were fit to each outcome. Odds of using the 3GP were 3.25 (95%CI: 1.38–7.67, p=.007) times higher for each unit increase in confidence. For each unit improvement in access and knowledge, physicians had 1.69 (1.17–2.43, p=.005) and 1.41 (1.17–1.71, p<.001) times higher odds of using genetic testing, respectively.

Odds of correctly identifying scenario 1 increased with more recent graduation [OR=1.37 (1.15–1.64) for every 5 year increase in graduation year, p<.001], higher knowledge [OR=1.41 (1.14–1.75), p=.002], and higher confidence in identification [OR=2.62 (1.45–4.73). Higher knowledge [OR=1.31 (1.10–1.55), p=.003] and higher confidence [OR=1.89 (1.20–2.96), p=.006] were also associated with higher odds of correctly identifying scenario 2.

Discussion

This study examined physician identification of HCs in rural Appalachia. Few physicians used a 3GP to collect family history information. This is concerning, due to its importance in identifying those at highest risk and the number of recommendations for collection of comprehensive family history information.[6, 16, 17] This may be partly due to a belief that patients are unreliable in reporting cancer family history or PCP time concerns. Yet, patients are reasonably accurate[35] and once a 3GP is completed, only brief updates are needed on subsequent visits. Further, consistent with other studies, use of cancer genetic testing was low, with less than half reporting any patients with genetic testing—even including conditions like neurofibromatosis. Also, many physicians (30%) did not identify the HBOC-relevant scenario. HBOC is perhaps one of the best known cancers and has received much attention in the media. Yet, more physicians appeared to identify the HBOC-relevant scenario than the HNPCC-relevant scenario. We suspect that there is less familiarity with hereditary colon cancer, especially as few physicians reported patients with HNPCC mutations. Thus, even for patients presenting with a strong family history of cancer, many physicians may not recognize the family history as a threat and could potentially dissuade patients from further cancer risk assessment and management.

We expected that rural and Appalachian physicians would have more challenges to identifying HCs due to more limited access to genetic services, but we saw no impact of rurality. Only one outcome evidenced any impact of Appalachian county of residence: genetic testing, and this did not remain significant in the multivariate model due to the effect of access. The lack of genetic testing does not appear to be due to differences in family history collection or ability to identify a HC family in rural and Appalachian physicians. In fact, rural and Appalachian physicians may have an advantage. Although they do not differ in their collection of a 3GP, rural Appalachian physicians may be able to better identify HCs due to an increased likelihood that members of the same extended family will see the same primary care physician over a long time period.[12]

In spite of the lack of findings for rural and Appalachian physicians, other findings emerged. Consistent with prior research, we found that physicians who graduated more recently were

more likely to accurately identify the HBOC relevant scenario than those who graduated longer ago. Physicians in practice longer may have more difficulty staying abreast of recent developments in genetic testing. In addition, psychosocial variables played a role in identification of HCs. Knowledge did not appear to be optimal, with no physicians responding correctly to all 10 questions, and knowledge predicted reporting a patient with genetic testing and correct identification of both scenarios. Increasing knowledge should increase the identification of HCs. In addition to knowledge, physicians need favorable attitudes toward identification of HCs. The factor 'confidence' and, to a lesser extent, the factor 'importance' played key roles in the identification of HCs. Higher confidence was associated with use of a 3GP and correct identification of the scenarios. Increasing knowledge and confidence are needed to improve physician identification of HCs.

Strengths and limitations to the current study should be noted. First, the wording of items in the survey may have influenced physician responses. Rather than asking physicians the number of individuals, we asked physicians if they had any patients who had genetic testing, and this may have lacked sensitivity to determine if access issues were a deterrent to genetic testing. Yet, asking physicians the number of individuals who had each type of testing may have been too time consuming (lowering our response rate) and may have lacked accuracy. One strength of our method is that we surveyed the diversity of types of HCs. Second, the number of physicians available to sample in some strata was small. To compensate for this small number, we could have adjusted our definition of rural by changing the range of RUCCs; however, our goal was to examine the most rural of areas. Our goals notwithstanding, the small sample size may have reduced the comparability of groups. Also, although our response rate is not ideal, it is comparable to other studies of mailed surveys to family physicians. In addition, we were able to examine a number of key factors associated with the identification of HC by physicians attending an underserved population. Finally, we do not know the age of the patient population seen by physicians in the study; thus, the adult-onset disorders may be less relevant to some physicians.

Conclusion

In sum, we found that the identification of HCs was less than optimal. In spite of our predictions about physicians practicing in rural and Appalachian Kentucky and Ohio, we found that they did not differ in identification of HCs from those practicing in more urban and non-Appalachian locations. However, physician's perception of access to genetic testing services was important, and this would likely be a greater challenge for underserved populations, including rural Appalachians. Research is needed to understand what these physicians perceive as access barriers. In addition, psychosocial factors play a key role in the identification of HCs. Knowledge and confidence in the ability to identify HCs are critical to both obtaining a 3GP and interpreting it. These results argue for increased educational efforts to improve physician knowledge of HCs, including practice in the interpretation of family history to build confidence, training in initial family history collection and periodic updating, and increased availability and increased awareness of availability of genetic services.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Table 1

Scale Development

Factor Analysis for Identification of Hereditary Cancer	**Factor Loadings**
1. Have you heard about testing for inherited susceptibility to cancer?	Dropped
Component 1: Confidence (Cronbach alpha=.87) (1=not at all to 5=extremely)	
2. How **knowledgeable** would you rate yourself in **identifying** individuals with familial/hereditary cancer syndromes?	.85
3. How **confident** are you in your ability to **identify** individuals with familial/hereditary cancer syndromes?	.82
4. How **comfortable** would you rate yourself in **identifying** individuals with familial/hereditary cancer syndromes?	.88
Component 2: Importance (Cronbach alpha=.83)	
5. How **important** is it for you to **identify** individuals with familial/hereditary cancer syndromes?	.82
6. How **effective** is **identifying** individuals with familial/hereditary cancer syndromes in controlling cancer?	.67
7. To what extent do your patients **need** to be **identified** if they have a familial/hereditary cancer syndrome?	.87
8. To what extent do you feel it is your **responsibility** to **identify** individuals with familial/hereditary cancer syndromes?	.74
Factor Analysis for Knowledge Items (Cronbach alpha=.91)	
1. Approximately 10% of all cancers are hereditary. (True)	.74
2. If a woman is positive for a mutation associated with a hereditary cancer syndrome but does not develop cancer, her child may also have that mutation. (True)	.55
3. All cancer is the result of changes in genetic material. (True)	.90
4. In hereditary non-polyposis colon cancer families, colon cancer tends to occur at an older age in each subsequent generation. (False)	.68
5. Individuals with hereditary non-polyposis colon cancer tend to have earlier onset cancers than individuals with familial adenomatous polyposis. (False)	.64
6. If an individual has early-onset colon cancer but has no family history, s/he may have hereditary non-polyposis colon cancer. (True)	.62
7. Four items were relevant to hereditary breast-ovarian cancer, “Cancers with a strong inherited component can occur in both breasts. (True)	.90
8. If a woman inherits a BRCA1 or BRCA2 (hereditary breast-ovarian cancer) mutation from her father, she has the same chance of developing breast or ovarian cancer as if she had inherited the mutation from her mother. (True)	.91
9. Even if a woman has a mutation in BRCA1, she may not develop cancer. (True)	.86
10. A BRCA1 or BRCA2 mutation is most likely suspected in a woman with breast cancer who has a family history of sarcoma and leukemia. (False)	.49